

#4

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/883,797

DATE: 11/27/2001

TIME: 12:54:48

Input Set : N:\Crf3\RULE60\09883797.raw

Output Set: N:\CRF3\11272001\I883797.raw

1 <110> APPLICANT: Jaworski, Jan G.
 2 Post-Beittenmiller, Martha A.
 3 Todd, James
 4 <120> TITLE OF INVENTION: FATTY ACID ELONGASES
 5 <130> FILE REFERENCE: 07148/064001
 6 <140> CURRENT APPLICATION NUMBER: 09/883,797
 7 <141> CURRENT FILING DATE: 2001-06-18
 8 <150> PRIOR APPLICATION NUMBER: 08/868,373
 9 <151> PRIOR FILING DATE: 1997-06-03
 10 <160> NUMBER OF SEQ ID NOS: 22
 11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 14 <211> LENGTH: 1560
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Arabidopsis thaliana
 17 <400> SEQUENCE: 1

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20	ggacttcaca actcttgcaa cgtgaccacc attctcttct tcttaattat tcttccttta	180
21	accggaaccg tgcgtgttca gctaaccggt ctaacgttcg atacgtttctc tgagctttgg	240
22	tctaaccagg cggttcaact cgacacggcg acgagactta cctgcttggt tttcctctcc	300
23	ttcgttttga cctctacgt ggctaaccgg tctaaaccgg tttacctagt ggatttctcc	360
24	tgctacaaac cggaagacga gcgtaaaata tcagtagatt cgttcttgac gatgactgag	420
25	gaaaatggat cattcaccga tgacacgggt cagttccagc aaagaatctc gaaccgggcc	480
26	ggtttgagg acgagacgta tctgccacgt ggcataactt caacgcccc gaagctaaat	540
27	atgtcagagg cagtgccga agctgaagcc gttatgtttg gagccttaga ttccctcttc	600
28	gagaaaaccg gaattaaacc ggccgaagtc ggaatcttga tagtaaactg cagcttattc	660
29	aatccgacgc cgtctctatc agcgatgac gtgaaccatt acaagatgag agaagacatc	720
30	aaaagttaca acctcggagg aatgggttgc tccgcgggat taatctcaat cgatctcgct	780
31	aacaatctcc tcaaagcaaa cctaattct tacgctgtcg tggtaagcac ggaaaacata	840
32	accctaaact ggtacttcgg aaatgaccgg tcaatgtctc tctgcaactg catcttccga	900
33	atgggaggag ctgcgattct cctctctaac cgccgtcaag accggaagaa gtcaaagtac	960
34	tcgctggtca acgtcgttcg aacacataaa ggatcagacg acaagaacta caattgcgtg	1020
35	taccagaagg aagacgagag aggaacaatc ggtgtctctt tagctagaga gctcatgtct	1080
36	gtcgccggag acgctctgaa aacaaacatc acgactttag gaccgatggt tcttccattg	1140
37	tcagagcagt tgatgttctt gatttccctg gtcaaaagga agatgttcaa gttaaaagtt	1200
38	aaaccgtata ttccggattt caagctagct ttccagcatt tctgtattca cgcaggagggt	1260
39	agagcggttc tagacgaagt gcagaagaat cttgatctca aagattggca catggaacct	1320
40	tctagaatga ctttgacag atttggtaac acttcagagta gctcgtttg gtatgagatg	1380
41	gcttataccg aagctaaggg tcgggttaaa gctggtgacc gactttggca gattgcgttt	1440
42	ggatcgggtt tcaagtgtaa tagtgcggtt tggaaagcgt tacgaccggt ttccgacggag	1500
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46 <211>	LENGTH: 520	
47 <212>	TYPE: PRT	
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53              20              25              30
54  Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val
55              35              40              45
56  Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val
57              50              55              60
58  Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp
59      65              70              75              80
60  Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu
61              85              90              95
62  Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys
63              100             105             110
64  Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg
65              115             120             125
66  Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Glu Asn Gly Ser
67              130             135             140
68  Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala
69      145             150             155             160
70  Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro
71              165             170             175
72  Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Ala Val Met
73              180             185             190
74  Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala
75              195             200             205
76  Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro
77              210             215             220
78  Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile
79      225             230             235             240
80  Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser
81              245             250             255
82  Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala
83              260             265             270
84  Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn
85              275             280             285
86  Asp Arg Ser Met Leu Leu Cys Asn Cys Ile Phe Arg Met Gly Gly Ala
87              290             295             300
88  Ala Ile Leu Leu Ser Asn Arg Arg Gln Asp Arg Lys Lys Ser Lys Tyr
89      305             310             315             320
90  Ser Leu Val Asn Val Val Arg Thr His Lys Gly Ser Asp Asp Lys Asn
91              325             330             335
92  Tyr Asn Cys Val Tyr Gln Lys Glu Asp Glu Arg Gly Thr Ile Gly Val
93              340             345             350
94  Ser Leu Ala Arg Glu Leu Met Ser Val Ala Gly Asp Ala Leu Lys Thr
95              355             360             365
96  Asn Ile Thr Thr Leu Gly Pro Met Val Leu Pro Leu Ser Glu Gln Leu
97      370             375             380
98  Met Phe Leu Ile Ser Leu Val Lys Arg Lys Met Phe Lys Leu Lys Val

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102     His Ala Gly Gly Arg Ala Val Leu Asp Glu Val Gln Lys Asn Leu Asp
103                                     420      425      430
104     Leu Lys Asp Trp His Met Glu Pro Ser Arg Met Thr Leu His Arg Phe
105                                     435      440      445
106     Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Met Ala Tyr Thr Glu
107                                     450      455      460
108     Ala Lys Gly Arg Val Lys Ala Gly Asp Arg Leu Trp Gln Ile Ala Phe
109     465                                     470      475      480
110     Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Pro
111                                     485      490      495
112     Val Ser Thr Glu Glu Met Thr Gly Asn Ala Trp Ala Gly Ser Ile Asp
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121 <400> SEQUENCE: 3
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124     caagatctcc aaaactttta cctctactta caaaacaacc acacatctct aaccatgttc      180
125     ttcttttacc tcgctctcgg gtcgactctt tacctcatga cccggcccaa acccgtttat      240
126     ctggttgact ttagctgcta cctcccacgg tcgcatctca aagccagcac ccagaggatc      300
127     atgcaacacg taaggcttgt acgagaagca ggcgcgtgga agcaagagtc cgattacttg      360
128     atggacttct gcgagaagat tctagaacgt tccggtctag gccaagagac gtacgtaccc      420
129     gaaggtcttc aaactttgcc actacaacag aatttggtctg tatcacgtat agagacggag      480
130     gaagttatta ttggtgcggt cgataatctg ttctgcaaca cgggaataag ccctagtgat      540
131     ataggtatat tgggtggtgaa ttcaagcact tttaatccaa caccttcgct atcaagtatc      600
132     ttagtgaata agtttaaact tagggataat ataaagagct tgaatcttgg tgggatgggg      660
133     tgtagcgtcg gagtcatcgc tatcgatgcg gctaagagct tgttacaagt tcatagaaac      720
134     acttatgctc ttgtggtgag cacggagaac atcaactcaa acttgtacat gggtacaac      780
135     aaatcaatgt tggttacaaa ctgtttggtc cgtatagggt gggccgcgat tttgctttct      840
136     aaccggtcta tagatcgtaa acgcgcaaaa tacgagcttg ttcacaccgt gcgggtccat      900
137     accgagcag atgaccgatc ctatgaatgt gcaactcaag aagaggatga agatggcata      960
138     gttggggttt ccttgtaaaa gaacttacct atggtagctg caagaaccct aaagatcaat      1020
139     atcgcaactt tgggtccgct tgttcttccc ataagcgaga agtttcactt ctttgtgagg      1080
140     ttctgttaaaa agaagtttct caaccccaag ctaaagcatt acattccgga tttcaagctc      1140
141     gcattcgagc atttctgtat ccatgcgggt ggtagagcgc taattgatga gatggagaag      1200
142     aatcttcacg taactccact agacgttgag gcttcaagaa tgacattaca caggtttggt      1260
143     aatacctctt cgagctccat ttggtacgag ttggcttaca cagaagccaa aggaaggatg      1320
144     acgaaaggag ataggatttg gcagatttgc ttggggctcag gttttaagtg taatagttca      1380
145     gtttggttgg ctcttcgtaa cgtcaagcct tctactaata atccttggga acagtgtcta      1440
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148 <210> SEQ ID NO: 4
149 <211> LENGTH: 493

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157 Val Glu Ala Ser Arg Leu Ser Thr Gln Asp Leu Gln Asn Phe Tyr Leu
158 35 40 45
159 Tyr Leu Gln Asn Asn His Thr Ser Leu Thr Met Phe Phe Leu Tyr Leu
160 50 55 60
161 Ala Leu Gly Ser Thr Leu Tyr Leu Met Thr Arg Pro Lys Pro Val Tyr
162 65 70 75 80
163 Leu Val Asp Phe Ser Cys Tyr Leu Pro Pro Ser His Leu Lys Ala Ser
164 85 90 95
165 Thr Gln Arg Ile Met Gln His Val Arg Leu Val Arg Glu Ala Gly Ala
166 100 105 110
167 Trp Lys Gln Glu Ser Asp Tyr Leu Met Asp Phe Cys Glu Lys Ile Leu
168 115 120 125
169 Glu Arg Ser Gly Leu Gly Gln Glu Thr Tyr Val Pro Glu Gly Leu Gln
170 130 135 140
171 Thr Leu Pro Leu Gln Gln Asn Leu Ala Val Ser Arg Ile Glu Thr Glu
172 145 150 155 160
173 Glu Val Ile Ile Gly Ala Val Asp Asn Leu Phe Arg Asn Thr Gly Ile
174 165 170 175
175 Ser Pro Ser Asp Ile Gly Ile Leu Val Val Asn Ser Ser Thr Phe Asn
176 180 185 190
177 Pro Thr Pro Ser Leu Ser Ser Ile Leu Val Asn Lys Phe Lys Leu Arg
178 195 200 205
179 Asp Asn Ile Lys Ser Leu Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
180 210 215 220
181 Val Ile Ala Ile Asp Ala Ala Lys Ser Leu Leu Gln Val His Arg Asn
182 225 230 235 240
183 Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Leu Tyr
184 245 250 255
185 Met Gly Asn Asn Lys Ser Met Leu Val Thr Asn Cys Leu Phe Arg Ile
186 260 265 270
187 Gly Gly Ala Ala Ile Leu Leu Ser Asn Arg Ser Ile Asp Arg Lys Arg
188 275 280 285
189 Ala Lys Tyr Glu Leu Val His Thr Val Arg Val His Thr Gly Ala Asp
190 290 295 300
191 Asp Arg Ser Tyr Glu Cys Ala Thr Gln Glu Glu Asp Glu Asp Gly Ile
192 305 310 315 320
193 Val Gly Val Ser Leu Ser Lys Asn Leu Pro Met Val Ala Ala Arg Thr
194 325 330 335
195 Leu Lys Ile Asn Ile Ala Thr Leu Gly Pro Leu Val Leu Pro Ile Ser
196 340 345 350
197 Glu Lys Phe His Phe Phe Val Arg Phe Val Lys Lys Lys Phe Leu Asn
198 355 360 365

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199      Pro Lys Leu Lys His Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His
200          370                      375                      380
201      Phe Cys Ile His Ala Gly Gly Arg Ala Leu Ile Asp Glu Met Glu Lys
202          385                      390                      395                      400
203      Asn Leu His Leu Thr Pro Leu Asp Val Glu Ala Ser Arg Met Thr Leu
204          405                      410                      415
205      His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
206          420                      425                      430
207      Tyr Thr Glu Ala Lys Gly Arg Met Thr Lys Gly Asp Arg Ile Trp Gln
208          435                      440                      445
209      Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala
210          450                      455                      460
211      Leu Arg Asn Val Lys Pro Ser Thr Asn Asn Pro Trp Glu Gln Cys Leu
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239      cctcttgtac ttccattaaa agagaagcta gccttcttta ttacttttgt caagaagaag      1140
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248 <210> SEQ ID NO: 6
249 <211> LENGTH: 504

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VERIFICATION SUMMARY

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